

Application No. 08/477,316
Attorney's Docket No. 028723-060

1
F wherein the chromosomal material is present in a morphologically identifiable cell nucleus;
allowing said probe to bind to said targeted chromosomal material; and detecting said bound
probe, wherein bound probe is indicative of the presence of target chromosomal material.

2
F 2 48. (Three Times Amended) A method of staining targeted interphase chromosomal
material based upon a nucleic acid segment employing a unique sequence high complexity
nucleic acid probe of greater than about 40 kb, wherein said targeted chromosomal material is
a genetic rearrangement associated with at least one chromosome in humans, said method
comprising contacting said chromosomal material with a unique sequence high complexity
nucleic acid probe of greater than about 40 kb, wherein the chromosomal material is present in
a morphologically identifiable cell nucleus; allowing said probe to bind to said targeted
chromosomal material; and detecting said bound probe, wherein bound probe is indicative of
the presence of target chromosomal material.

3
F 3 50. (Three Times Amended) A method of staining targeted interphase chromosomal
material based upon a nucleic acid segment employing a unique sequence high complexity
nucleic acid probe of greater than about 50,000 bases, wherein said targeted interphase
chromosomal material is a genetic rearrangement associated with at least one chromosome in
humans, said method comprising contacting said interphase chromosomal material with a
unique sequence high complexity nucleic acid probe of greater than about 50,000 bases,
wherein the chromosomal material is present in a morphologically identifiable cell nucleus;
allowing said probe to bind to said targeted interphase chromosomal material; and detecting
said bound probe, wherein bound probe is indicative of the presence of target interphase
chromosomal material.

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[Please add the following new claims:

-- 12 59. The method of claim 48², wherein complexity of the unique sequence high complexity nucleic acid probe is greater than about 100,000 bases.

F⁴ 13 60. The method of claim 50³, wherein complexity of the unique sequence high complexity nucleic acid probe is greater than about 100,000 bases. - -